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providing a sample potentially containing one or more target nucleotide sequences with a plurality of sequence differences;

providing a plurality of oligonucleotide probe sets, each set characterized by (a) a first oligonucleotide probe, having an oligonucleotide target-specific portion and an oligonucleotide addressable array-specific portion and (b) a second oligonucleotide probe, having an oligonucleotide target-specific portion and a detectable reporter label, wherein the oligonucleotide probes in a particular set are suitable for ligation together when hybridized adjacent to one another on a corresponding target nucleotide sequence, but have a mismatch which interferes with such ligation when hybridized to any other nucleotide sequence present in the sample;

providing a ligase,

blending the sample, the plurality of oligonucleotide probe sets, and the ligase to form a mixture;

subjecting the mixture to one or more ligase detection reaction cycles comprising a denaturation treatment, wherein any hybridized oligonucleotides are separated from the target nucleotide sequences, and a hybridization treatment, wherein the oligonucleotide probe sets hybridize at adjacent positions in a base-specific manner to their respective target nucleotide sequences, if present in the sample, and ligate to one another to form a ligated product sequence containing (a) the addressable array-specific portion, (b) the target-specific portions connected together, and (c) the detectable reporter label, and, wherein the oligonucleotide probe sets may hybridize to nucleotide sequences in the sample other than their respective target nucleotide sequences but do not ligate together due to a presence of one or more mismatches and individually separate during the denaturation treatment;

providing a solid support with different capture oligonucleotides immobilized at particular sites, wherein the capture oligonucleotides have nucleotide sequences complementary to the addressable array-specific portions;

contacting the mixture, after said subjecting, with the solid support under conditions effective to hybridize the addressable array-specific portions to the capture oligonucleotides in a base-specific manner, thereby capturing the addressable array-specific portions on the solid support at the site with the complementary capture oligonucleotide; and

detecting the reporter labels of ligated product sequences captured to the solid support at particular sites, thereby indicating the presence of one or more target

nucleotide sequences in the sample, wherein sequences differing by one or more single-base changes, insertions, deletions, or translocations are discriminated from one another during the ligase detection reaction and the discriminated sequences are detected as a result of capture on the solid support.

151. A method for identifying one or more of a plurality of sequences differing by one or more single-base changes, insertions, deletions, or translocations in a plurality of target nucleotide sequences comprising:

providing a sample potentially containing one or more target nucleotide sequences with a plurality of sequence differences;

providing a plurality of oligonucleotide probe sets, each set characterized by (a) a first oligonucleotide probe, having an oligonucleotide target-specific portion and an oligonucleotide addressable array-specific portion and (b) a second oligonucleotide probe, having an oligonucleotide target-specific portion and a detectable reporter label, wherein the oligonucleotide probes in a particular set are suitable for ligation together when hybridized adjacent to one another on a corresponding target nucleotide sequence under a single set of ligase detection reaction conditions, but have a mismatch which interferes with such ligation when hybridized to any other nucleotide sequence present in the sample;

providing a ligase,

blending the sample, the plurality of oligonucleotide probe sets, and the ligase to form a mixture;

subjecting the mixture to one or more ligase detection reaction cycles comprising a denaturation treatment, wherein any hybridized oligonucleotides are separated from the target nucleotide sequences, and a hybridization treatment, wherein the oligonucleotide probe sets hybridize at adjacent positions in a base-specific manner to their respective target nucleotide sequences, if present in the sample, and ligate to one another to form a ligated product sequence containing (a) the addressable array-specific portion, (b) the target-specific portions connected together, and (c) the detectable reporter label, and, wherein the oligonucleotide probe sets may hybridize to nucleotide sequences in the sample other than their respective target nucleotide sequences but do not ligate together due to a presence of one or more mismatches and individually separate during the denaturation treatment;

providing a solid support with different capture oligonucleotides immobilized at particular sites, wherein the capture oligonucleotides have nucleotide sequences complementary to the addressable array-specific portions;

contacting the mixture, after said subjecting, with the solid support under conditions effective to hybridize the addressable array-specific portions to the capture oligonucleotides in a base-specific manner, thereby capturing the addressable array-specific portions on the solid support at the site with the complementary capture oligonucleotide; and

detecting the reporter labels of ligated product sequences captured to the solid support at particular sites, thereby indicating the presence of one or more target nucleotide sequences in the sample.

Please amend claims 1, 58-59, and 138 as follows:

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1. (Thrice Amended) A method for identifying one or more of a plurality of sequences differing by one or more single-base changes, insertions, deletions, or translocations in a plurality of target nucleotide sequences comprising:

providing a sample potentially containing one or more target nucleotide sequences with a plurality of sequence differences;

providing a plurality of oligonucleotide probe sets, each set characterized by (a) a first oligonucleotide probe, having an oligonucleotide target-specific portion and an oligonucleotide addressable array-specific portion[, wherein the oligonucleotide addressable array-specific portion is comprised of an oligonucleotide sequence that is distinct from the oligonucleotide sequence of the target-specfic portion,] and (b) a second oligonucleotide probe, having an oligonucleotide target-specific portion and a detectable reporter label, wherein the oligonucleotide probes in a particular set are suitable for ligation together when hybridized adjacent to one another on a corresponding target nucleotide sequence, but have a mismatch which interferes with such ligation when hybridized to any other nucleotide sequence present in the sample;

providing a ligase,

blending the sample, the plurality of oligonucleotide probe sets, and the ligase to form a mixture;

subjecting the mixture to one or more ligase detection reaction cycles comprising a denaturation treatment, wherein any hybridized oligonucleotides are separated from the target nucleotide sequences, and a hybridization treatment, wherein the oligonucleotide probe sets hybridize at adjacent positions in a base-specific manner to their respective target nucleotide sequences, if present in the sample, and ligate to one another to form a ligated product sequence containing (a) the addressable array-specific portion, (b) the target-specific portions connected together, and (c) the detectable reporter label, and, wherein the oligonucleotide probe sets may hybridize to nucleotide sequences in the sample other than their respective target nucleotide sequences but do not ligate together due to a presence of one or more mismatches and individually separate during the denaturation treatment;

providing a solid support with different capture oligonucleotides immobilized at particular sites, wherein the capture oligonucleotides have nucleotide sequences complementary to the addressable array-specific portions;

contacting the mixture, after said subjecting, with the solid support under conditions effective to hybridize the addressable array-specific portions to the capture oligonucleotides in a base-specific manner, thereby capturing the addressable array-specific portions on the solid support at the site with the complementary capture oligonucleotide; and

detecting the reporter labels of ligated product sequences captured to the solid support at particular sites, thereby indicating the presence of one or more target nucleotide sequences in the sample, wherein the oligonucleotide probe sets are configured so that the addressable array-specific portion is comprised of a nucleotide sequence which is distinct from that of the target-specific portions, in order to minimize hybridization between the target-specific portions and the capture oligonucleotides as well as between the target nucleotide sequence and the addressable array-specific portion.

57 ~~58~~. (Twice Amended) A method according to claim 56 ~~57~~, wherein the genetic disease [has] correlates with a known nucleotide sequence and is selected from the group consisting of 21 hydroxylase deficiency, cystic fibrosis, Fragile X Syndrome, Turner Syndrome, Duchenne Muscular Dystrophy, Down Syndrome, heart disease, single gene diseases, HLA typing, phenylketonuria, sickle cell anemia, Tay-Sachs Syndrome, thalassemia, Klinefelter's Syndrome, Huntington's Disease, autoimmune diseases, lipidosis, obesity defects, hemophilia, inborn error in metabolism, and diabetes.

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58 59. (Twice Amended) A method according to claim 1, wherein said method is used to detect cancer [having] which correlates with the presence of a known nucleotide sequence, including those [and] involving oncogenes, tumor suppressor genes, or genes involved in DNA amplification, replication, recombination, or repair.

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138. (Twice Amended) A kit for identifying one or more of a plurality of sequences differing by single-base changes, insertions, deletions, or translocations in a plurality of target nucleotide sequences comprising:

a ligase;

a plurality oligonucleotide probe sets, each characterized by (a) a first oligonucleotide probe, having an oligonucleotide target sequence-specific portion and an oligonucleotide addressable array-specific portion[, wherein the oligonucleotide addressable array specific portion is comprised of an oligonucleotide sequence that is distinct from the oligonucleotide sequence of the target-specific portion] and (b) a second oligonucleotide probe, having an oligonucleotide target sequence-specific portion and detectable reporter label, wherein the oligonucleotide probes in a particular set are suitable for ligation together when hybridized adjacent to one another on a respective target nucleotide sequence, but have a mismatch which interferes with such ligation when hybridized to any other nucleotide sequence, present in the sample; and

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a solid support with capture oligonucleotides immobilized at particular sites, wherein the capture oligonucleotides have nucleotide sequences complementary to the addressable array-specific portions, wherein the oligonucleotide probe sets are configured so that the addressable array-specific portion is comprised of a nucleotide sequence which is distinct from that of the target-specific portions, in order to minimize hybridization between the target-specific portions and the capture oligonucleotides as well as between the target nucleotide sequences and the addressable array-specific portion.

REMARKS

In view of the above amendments and the following remarks, reconsideration of the outstanding office action is respectfully requested.